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Result
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Maximum Match 100%
. Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Minimum DB seq length: 0
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Perfect score:
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                                                                                                                                                                                    Score
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69.5
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1: sp_archea:*
2: sp_bacteria:
3: sp_fungi:*
4: sp_human:*
5: sp_invertebb
6: sp_mammal:*
7: sp_mhc:*
8: sp_organelie
9: sp_phage:*
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Match
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418
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sp_phage:*
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196.351 Million cell updates/sec
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OBSSXO dictyosteli
OBSSXO dictyosteli
OBSSE4 homo sapien
OBNE56 leiBhmania
OB11c6 white spot
OBVAY1 white spot
OBVAY1 white spot
OBVAY2 drosophila
OBTUS OTYZA SATIV
OBSTUS OTYZA SATIV
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P79994 a	005061 4	023073 c	0	\boldsymbol{T}	σ			Q9upq1 h	Q8w0a0 o	Q02090	Q9awx4	Q8s826 •	Q96u39 n		3	Q9suf7 a	ш		Q8vy68	Q962J9 p	Q9cln6	Q961u0 h	094043 ca		Q9v995 d:	Q24486 d:	Q91gv0 (001844 ci
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ALIGNMENTS

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263 2 96SE4 96SE4;	204 FA 70 GG	Query Match Best Local Similarity Matches 23; Conser 10 YLFIYFLSY	SEQUENCE	Submitted ("Sequence a	Lehmann R.,	Gloeckner G.,		CEOURNCE FR	NCBI_TaxID=44689;	Eukaryota;	Dictyosteli	01-JUN-2002	01-JUN-2002	01-JUN-2002	0855X0:	OBSSYO VO	LT 1	
GGFGNGGG 270 GFRELIMINARY;	FAFVSFDSEDAVEKA-I GGTADTGG 77	20.2%; ilarity 33.8%; Conservative FIYFLSYSLGDRARLC	EMBL; ACII3380; AAL92217.1; ~. SEQUENCE 299 AA; 31509 MW;	Submitted (MAR-2002) to the	"Sequence and Analysis of Chromosome 2 of Dictyostelium.		Eichinger I	On N.A.	FROM N A	44689;	14	Dictyostelium discoideum ((TrEMBLrel. 21,	(TrEMBLrel. 21,	· White was a	DEST.TMTNARY.		
PRT; 2	ALTGTKFEGRE	; Score 84.5; 1; Pred. No. 0.0; 13; Mismatches	Σ	e EMBL/GenE	Chromosome	Parra G., April J.F., Guigo R.,	, Szafransk				yosteliida;	(Slime mold).	1, Last annotation update)	, Last sequ	, Created)	,			
2724 AA.	: !IQVERSQRG	Score 84.5; DB 5 Pred. No. 0.057; ; Mismatches 3 KTKQQQKEQQILRQSEV	F2F14958E9C08B66	EMBL/GenBank/DDBJ databases	2 of Dict	oril J.F.,	1 K., Pac				Dictyost		otation up	Last sequence update)			799 AA		
	: :	; Length 299; 1; Indels 1; LFRSETLRKTGKKGRRWG	6 CRC64;	databases.	Chromosome 2 of Dictyostelium.";	`. ×	п				elium.		date)	te)					
	262	1;			•	•													

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Matches 24
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01-OCT-2000
01-OCT-2000
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Mammalia; E
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01-DEC-2001
01-MAR-2002
                                       Genome Res. 8:135-145(1998).
EMBL; AL157415; CAB75639.1; -.
HSSP; P17119; 3KAR.
InterPro; IPR001752; kinesin_motor.
Pfam; PF00225; kinesin; 1.
SMART; SM00129; KISC; 1.
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Barrell B.
PROSITE; PS00411; KINESIN MOTOR DOMAIN1; 1.

PROSITE; PS50067; KINESIN MOTOR DOMAIN2; 1.

ATP-binding; Coiled coil; Microtubules; Motor protein.

SEQUENCE 1254 AA; 132206 MW; 79350B2FBCB2BZOA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pfam; PF00270; DEAD; 1.
Pfam; PF00476; DNA_PO1_A; 1.
Pfam; PF00271; helicase_C; 1.
PROSITE; PS00447; DNA_POLYMERASE_A; UNKNOWN_1.
ATP-binding; Helicase.
SEQUENCE 2724 AA; 305148 MW; 305888663614E6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Abbas A.R., Linn S.M.;
"Homo sapiens polymerase (DN Submitted (APR-2001) to the EMBL; AY032677; AAK39635.1;
                                                                                                    "A physical map of the Leishmania
                                                                                                                Ivens A.C.,
Smith D.F:;
                                                                                                                                  MEDLINE-98146435;
                                                                                                                                                STRAIN-FRIEDLIN,
                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                             Submitted
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                                                                                                                                                                                                                                        Leishmania major.
Eukaryota; Euglenozoa;
NCBI_TaxID=5664;
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InterPro; IPR001098; DNA_pol.
InterPro; IPR001650; Helicase_C.
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; Metazoa; Chordata;
Eutheria; Primates;
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(TrEMBLrel.)
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Best Local :
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                                      Yang F., E
Submitted
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01-MAR-2002 (TrEMBLrel.
01-MAR-2002 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

MEDLINE=21342572; PubMed=11448154;

Wan Hulten M.C.W., Witteveldt J., Peters S

Tarchini R., Fiers M., Sandbrink H., Lankh

"The white spot syndrome virus DNA genome
Virology 286:7-22(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-DEC-2001 (TREMBLIE 1.19,
01-DEC-2001 (TREMBLIE 1.19,
01-DEC-2001 (TREMBLIE 1.19,
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                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE-21548311; PubMed-11689662;
Yang F., He J., Lin X., Li Q., Pan
                                                                                                                                                                                                                                                                        White spot syndrome vi
Viruses; unclassified
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Tarchini R., Fiers M., Sandbrink H., Lankhorst
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ
EMBL; AF369029; AAK77788 1;
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                                                                                                                                    virus
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                                      (DEC-2000)
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Vlak J.M.;
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                                              InterPro; IPR001410; DEAD.
InterPro; IPR001650; Helicas
Pfam; PF00270; DEAD; 1.
Pfam; PF00271; DEADc; 1.
SMART; SM00487; DEXDC; 1.
SMART; SM00490; HELICCc; 1.
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STRAIN=CV. COLUMBIA;
Federspiel N.A., Palm C.J., Conway A.B., Kv
Rederspiel N.A., Palm C.J., Conway A.B., Kv
Au M., Araujo R., Buehler E., Dewar K., Fer
Au M., Araujo R., Buehler E., Davia R.W.,
Oji O., Osborne B.I., Shinn P., Sun H., Toj
Oji O., Osborne B.I., Theologis A., Davia R.W.,
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Lo C.F., K
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Spermatophyta; Magnoliophyta; eudicotyta; edicots; core eudicots; Rosid

eurosids_II; Brassicales; Brassicaceae; Arabidopsis.
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EMBL; AF332093; AAL33242.1; -.
EMBL; AF440570; AAL89162.1; -.
SEQUENCE 486 AA; 51463 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tsai M.F., Yu H.T., Tzeng H.F., Leu J.H., Chou C.M., Huang C Wang C.H., Lin J.Y., Kou G.H., Lo C.F.;
"Identification and characterization of a shrimp white spot virus (WSSV) gene that encodes a novel chimeric polypeptide cellular-type thymidine kinase and thymidylate kinase.";
Virology 277:100-110(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Identification of a nucleocapsid protein (VP35) gene of shrimp spot syndrome virus and characterization of the motif important targeting VP35 to the nuclei of transfected insect cells."; Virology 293:44-53(2002).
                                                                                                                                                                                                   EMBL; AC002291; AAC00620.1; HSSP; Q58083; 1HV8.
                                                                                                                                                                                                                                            Yu G., Ecker J., Theologis A., Davis R.W.;
Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=3702;
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MEDLINE=21844071;
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H., Huang C.J., Chou
  93503 MW;
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Pred. No. 2.3;
19; Mismatches
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Feng J., Kim C., Li Y.,
Toriumi M., Vysotskaia V.S.
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Matches 20
                             FlyBase; FBgn0028431; Glu-RIB
InterPro, IPR001828; ANT_recep,
InterPro; IPR001320; Ion_glu_i
InterPro; IPR001322; K+Channe.
InterPro; IPR001311; SBP/glu_i
                                                                                                                                                                                                            Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Trosophila melanogaster."; Science 287:2185-2195(2000).
EMBL; AE003552; AAF50306.1; -.
HSSP; P19491; 1GR2.
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Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscc
Ephydroidea; Drosophilidae; Drosophila.
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01-MAY-2000 (TrEMBLrel.
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Ion_glu_receptor.
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Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18;
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RESULT OF THE PROPERTY OF THE 
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Best Local S
Matches 17
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Best Local S
Matches 17
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ProDom; PD000500; Ion_c
SMART; SM00079; PBPe; I
SEQUENCE 1049 AA; 11
Q8RU52 PRELIMINARY; PRT; 1150 AA.
Q8RU52;
Q1-JUN-2002 (TrEMBLrel. 21, Created)
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
Q1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Putative copia-like retrotransposon hopscotch polyprotein.
QSJNBB0048022.20.
QYZA SATIVA (Japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poaceae;
Ehrhartoideáe; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    InterPro; IPR001320; Ion_glu_receptor.
InterPro; IPR001622; K+channel_pore.
InterPro; IPR0016131; SBP/glu_receptor.
Pfam; PF00060; 11g_chan; 1.
PRINTS; PR01582; KV33CHANNEL.
ProDom; PD000500; Ion_glu_receptor; 1.
SMART; SM00079; PBPe; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-WT BERLIN, AND CANTON S;
Voelkner M., Lenz-Boehme B., Fuchs S., Wismar J., Betz H., Schmitt "Novel glutamate receptor subunit genes of Drosophila melanogaster. Submitted (DEC-199) to the EMBL/GenBank/DDBJ databases.
EMBL; AJ251887; CAB64940.1; -.
EMBL; AJ251886; CAB64939.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ionotropic glutamate receptor subunit IB prec
GLU-RIB OR GLUR-IB OR CG4481.
Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Tracheata; He
Pterygota; Neoptera; Endopterygota; Diptera;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Q9TVG7;
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annual update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q9TVG7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Receptor; Signal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FlyBase; FBgn0028431; Glu-RIB.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          HSSP; P19491; 1GR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A. STRAIN-WT BERLIN,
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s; PR01582; KV33CHANNEL.
                                                                                                                                                                                                                                                                                                                                                                                                                     28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28
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17; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     LRKTKQQQKEQQILRQSEVLFRSETLRKTGKKGRRWGGQGGRGGTADTGGMF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LRKTKQQQKEQQILRQSEVLFRSETLRKTGKKGRRWGGQGGRGGTADTGGMF
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1095 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          26
1095
· 120782 »
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32.7%;
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32.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 70.5; I
Pred. No. 11;
6; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     6,
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Pred. No. 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          IONOTROPIC GLUTAMATE RECEPTOR W; EDDF0316A948C32E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRT;
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a; Brachycera;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1;
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RESULT 10
Q94E54
ID Q94E5
AC Q94E5
DT 01-DE
DT 01-DE
DT 01-DE
DT 01-DE
DT 01-BA
OC ENLAR
OC STRAI
RA SASAK
RT CLONE
RL SUDMI
RESULT 11
Q9SNU6
ID Q9SNU
AC Q9SNU
DT 01-MA
DT 01-MA
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Best Local
                                                                                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                                               Best
                                                                                                                                                                                                                                                                                      Submitted (FEB-2001) to the EMF
EMBL; AP003215; BAB62558.1; -.
InterPro; IPR004827; TF_bZIP.
Pfam; PF00170; bZIP; 1.
PROSITE; PS00036; BZIP_BASIC; U
SEQUENCE 203 AA; 21092 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.

STRAIN-CV. NIPPONBARE;
Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Kim M.M.
Overton II L.L., Bera J.J., Tsitrin T., Krol M.I., Jarrahi B.B.
Jin S.S., Koo H., Zismann V., Hsiao J., Blunt S., Vanaken S.S.,
Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B.,
Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser
Oryza sativa chromosome 10 BAC OSJNBb0048022 genomic sequence.
Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                      STRAIN-CV. NIPPONBARE;
Sasaki T., Matsumoto T., Yamar
Sasaki T., Imponbare(GA3)
"Oryza sativa nipponbare(GA3)
clone:OSJNBA0089K24.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza.
NCBI_TaxID-4530;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Oryza sativa (Rice).
Eukaryota; Viridiplantae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
01-JUN-2002 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Putative THY5 protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                               Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . Similarity
22; Conserv
                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                    SLGDRARLCLRK-----TKQQQKEQQ-----
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                                                                                                                 TLRQILKNTTAHAGKRGGGGGGKGGDGGGGG
                                                                                                                                                                        SAGDKEQNRLKRLLRNRVSAQQARERKKAYMTELEAKAKDLELRNAELEQRVSTLQNENN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LSYLLSSLAREILTQVVSIETAAELWRTLENMLCSQTENYHKMNSFSDEMAMTTTRKGRS
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                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
                                                                                                                                             -TGKKGRRWGGQGGRGGTADTGG
                                                                                                                                                                                                                                              16.5%;
26.4%;
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19,
21,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Created)
Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                                                                                                                          EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7;
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Pred. No. 15;
7; Mismatches
                                                                                                                                                                                                                                               Score 69; DB
Pred. No. 2.6;
                                                                                                                                                                                                                                                                                       UNKNOWN_1.
C796B3659CD9255F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                     genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Liliopsida;
                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                     DNA,
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                                                                                                                                                                                                                                                                                                                                                                                      chromosome 1,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              update)
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                                                                                                                                                                                                                                22;
                                                                                                                                                                                                                                                           Length 203
                                                                                                                                                                                                    -ILRQSEVLFRSETLRK----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Poaceae;
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Jarrahi B.B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1150;
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                                                                                                                                                                                                                                32;
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01-MAY-2000 01-MAY-2000 9DNS60

(TrEMBLrel.

13, 13,

Created) Last sequ

sequence

update)

PRELIMINARY;

PRT;

296

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Q9SNU6;

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RESULTATION OF THE PROPERTY OF
              RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Burton G.G., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA Brandon R.C., Boyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.F., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Fosler C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Meison D.R., Melson R.A., Mixon K., Nusskern D.R., Pacleb J.M.,
RA Meison D.R., Nelson R.A., Nixon K., Nusskern D.R., Pacleb J.M.,
RA Reinert K., Renington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Shue H.G., Siden-Kimser T. Stemeon M. Schuski M.B., Schih H.,
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q9W1J3;
Q9W1J3;
Q1-MAY-2000
Q1-MAY-2000
Q1-JUN-2002
CG5543 prote
CG5543.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Metazoa; l
Pterygota; Neoptera;
Ephydroidea; Drosoph;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          clone:P0538C01.";
Submitted (AUG-1999) to the EMBL/GenBank/DDBJ databases
EMBL; AP000391; BAA83351.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oryza sativa (Rice).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=20196006; PubMed=10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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Sasaki T., Matsumoto T.,
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ESTs AU077435(C12539).
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NY-2000 (TrEMBLrel. 13, 1
NY-2002 (TrEMBLrel. 21, I
3 protein (LD31556P).
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17; Conserv
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Neoptera; Endopterygota;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      296 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Drosophilidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   32558 MW; 3217A4F710A4FFD2 CRC64;
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ota; Diptera;
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a; Brachycera; Musc
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RA GONZALEZ M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
RA GONZALEZ M., GUARÍN H., Li P., Liao G., Miranda A., Mungall C.J.,
RA Nunco J., Pacleb J., Paragas V., Park S., Phouanenavong S., Wan K.,
RA YU C., Lewis S.E., Rubin G.M., Celniker S.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.
CC -!- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
DR EMBL; AE003462; AAF47065.1; -
DR EMBL; AE003462; AF47065.1; -
DR EMBL; AE0034628; CG5543.
DR InterPro; IPR001680; WD40.
PR F19Base; FB9n0034908; CG5543.
DR InterPro; IPR001680; WD40.
PR PINTS; PR001320. CT.
R CUPPT
                                                                                                                                                                                                                                                                                                                                   RESULT
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            Query Match
Best Local
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Best Local
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                                                SEQUENCE FROM N.A.
Wing R.A., Yu Y., Soderlund C.,
Wing R.A., Yu Y., Soderlund C.,
Saski C., Henry D., Oates R., Si
"Rice Genomic Sequence.";
Rice Genomic Sequence.";
Submitted (APR-2002) to the EMBL
Submitted (APR-2002) to the EMBL
EMBL; AC104428; AAM15780.1;
Homeobox; DNA-binding; Nuclear p
SEQUENCE 884 AA; 94539 MW; 1
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01-JUN-2002
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                                                                                                                                                                     Spermatophyta; Magnoliophyta; Ehrhartoideae; Oryzeae; Oryza, NCBI_TaxID=39947;
                                                                                                                                                                                                             Oryza sativa (japonica cultivar-group). Eukaryota; Viridiplantae; Streptophyta;
                                                                                                                                                                                                                                                                                                       Q8S5U8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wang Z.-Y. Wassarman D.A. Weinstock G.M., Weissenbach J., Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., Glubs R.A., Myers E.W., Rubin G.M., Venter J.C.; "The genome sequence of Drosophila melanogaster."; Science 287:2185-2195(2000).
                                                                                                                                                                                                                                       OJ1123F12.2.
                                                                                                                                                                                                                                                    Putative homeodomain protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE: PS00678; WD_REPEATS_1; 2.
PROSITE: PS50082; WD_REPEATS_2; 2.
PROSITE: PS50294; WD_REPEATS_REGION;
                                                                                                                                                                                                                                                                   01-JUN-2002
                                                                                                                                                                                                                                                                                                                        Q8S5U8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ARLCLRKTKQQQKEQQILRQSEV-----LFRSE---TLRKTGKKGRR----
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R., Tector C., Turner R., Venter E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    repeat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                        PRELIMINARY;
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            16.48;
                                                                                        to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           16.5%;
                                                                                                     d C., cac
R., Simmons
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                13;
                                                                                                                                                                                                                                                                  Last sequence up
                                                                                                                                                                                                                                                                                            Created)
            Score 68.5;
Pred. No. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 69; 1
Pred. No. 9
                                                                                                                                                                                                 Liliopsida;
                                                                                                                                                                                                                                                                                                                        PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                  81
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                                                   protein.
1F29B5DBAD0035F3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
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                                                                                                                                                                                                                                                                                                                        884
                                                                                                                    ٦.;
                                                                                                                                                                                                             Embryophyta; Tracheophyta;
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             5;
                                                                                                                               Kim H.-R.,
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                                                                                          databases
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;
                                                    CRC64;
                         Length
                                                                                                                                                                                                 Poaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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                                                                                                                                 Rambo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wang
                          884;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      62
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Conservative

Mismatches

14;

Indels

25;

Gaps

4.

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QBRISE
ID QBRIS
AC QBRIS
DT 01-JU
DT 01-JU
DT 01-JU
DT 01-JU
DE HYPOT
OS MUS m
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Best Local S
Matches 15
                                                                                                                                                                                       Query Match
Best Local (
                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JUN-2002 (TrEMBLrel. 21, Created)
01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
1-JUN-2002 (TrEMBLrel. 21, Last annotation update)
Hypothetical 48.0 kDa protein (Fragment).
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae,
                                                                                                                                                                                                                                                                                         Hypothetical protein.
                                                                                                                                                                                                                                                                                                                                       Strausberg R.;
Submitted (FEB-2002) to the EMBL/GenBank/DDBJ databases
EMBL; BC024127; AAH24127.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Q8R1S6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL; AJ003194;
NON_TER 1
SEQUENCE 165 i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-JUN-1998 (TrEMBLrel. 06, Created)
01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q8R1S6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-ATCC 393;
MEDLINE-98012962; PubMed-9352913;
Monddero V., Gosalbes M.J., Perez-Martinez G.;
"Catabolite repression in Lactobacillus casei ATCC393 is mediated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         050357;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    050357
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Firmicutes; Bacillus/Clostridium group; Lactobacillales;
Lactobacillaceae; Lactobacillus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CcpA & tnp genes (Fragment).
Lactobacillus casei.
                                                                                                                                                                                                                                                                                                                                                                                                                          TISSUE-LIVER;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=1582;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Bacteriol. 179:6657-6664(1997).
3L; AJ003194; CAA05974.1; -.
     43 QSEVLFRSETLRKTGKKGRRWGGQGGRGGTADTGG 77
                                                        20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              46
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                                                                                                      3 LSTHLFIYLFIYFLSYSLGDRARL-----
                                                                                                                                                            Similarity 20; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         l Similarity
15; Conserv
                                                   ISEHCFDLIFAFDEIVALGYRENVNLAQIRTFTEMDSHEEKVFRAVRETQEREAKAEMRR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QQNQQGTSENPAKVKPQTTGTGGSNGDRTGGTGGTGTTTETG 129
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RHWSGGGDGRG 56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ----GGQGGRG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LHVILSLFFLPLFPFSLSTSA-FCKRRWRQRQR----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LFIYLFIYFL---SYSIGDRARLCLRKTKQQQKEQQILRQSEVLFRSETLRKTGKKGRRW 63
                                                                                                                                                                                                                                                                429 AA; 47964 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             165 AA; 16851 MW;
                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRELIMINARY;
                                                                                                                                                       16.3%; Sco
21.1%; Pro
ative 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16.3%;
35.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 68; DB 2; Length 165; Pred. No. 2.8; 6; Mismatches 21; Indels
                                                                                                                                                                                  Score 68; DB 11; Length 429; Pred. No. 7.9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
                                                                                                                                                                                                                                                                40ABE6564EB1BBEA CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C54BDCC033EE93AC CRC64;
                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 165
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                                                                                                                                                          Indels
                                                                                                      ---CLRKTKQQQKEQQILR 42
                                                                                                                                                          22;
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Job time: 88 secs